

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Wynn, Thomas
Chiaramonte, Monica
Collins, Mary
Donaldson, Debra
Fitz, Lori
Neben, Tamlyn
Whitters, Matthew
Wood, Clive
- (ii) TITLE OF INVENTION: TREATMENT OF FIBROSIS BY ANTAGONISM OF IL-13
AND IL-13 RECEPTOR CHAINS
- (iii) NUMBER OF SEQUENCES: 9
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Genetics Institute, Inc.
 - (B) STREET: 87 CambridgePark Drive
 - (C) CITY: Cambridge
 - (D) STATE: MA
 - (E) COUNTRY: USA
 - (F) ZIP: 02140
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Brown, Scott A.
 - (B) REGISTRATION NUMBER: 32,724
 - (C) REFERENCE/DOCKET NUMBER: GI5268A2
- (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1525 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 256..1404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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GAATTCGGCA CGAGGGAGAG GAGGAGGGAA AGATAGAAAG AGAGAGAGAA AGATTGCTTG      60
CTACCCCTGA ACAGTGACCT CTCTCAAGAC AGTGCTTTGC TCTTCACGTA TAAGGAAGGA      120
AAACAGTAGA GATTCAATTT AGTGTCTAAT GTGGAAAGGA GGACAAAGAG GTCTTGTGAT      180
AACTGCCTGT GATAATACAT TTCTTGAGAA ACCATATTAT TGAGTAGAGC TTTCAGCACA      240
CTAAATCCTG GAGAA ATG GCT TTT GTG CAT ATC AGA TGC TTG TGT TTC ATT      291
              Met Ala Phe Val His Ile Arg Cys Leu Cys Phe Ile
                1             5             10

CTT CTT TGT ACA ATA ACT GGC TAT TCT TTG GAG ATA AAA GTT AAT CCT      339
Leu Leu Cys Thr Ile Thr Gly Tyr Ser Leu Glu Ile Lys Val Asn Pro
   15             20             25

CCT CAG GAT TTT GAA ATA TTG GAT CCT GGA TTA CTT GGT TAT CTC TAT      387
Pro Gln Asp Phe Glu Ile Leu Asp Pro Gly Leu Leu Gly Tyr Leu Tyr
   30             35             40

TTG CAA TGG AAA CCT CCT GTG GTT ATA GAA AAA TTT AAG GGC TGT ACA      435
Leu Gln Trp Lys Pro Pro Val Val Ile Glu Lys Phe Lys Gly Cys Thr
   45             50             55             60

CTA GAA TAT GAG TTA AAA TAC CGA AAT GTT GAT AGC GAC AGC TGG AAG      483
Leu Glu Tyr Glu Leu Lys Tyr Arg Asn Val Asp Ser Asp Ser Trp Lys
   65             70             75

ACT ATA ATT ACT AGG AAT CTA ATT TAC AAG GAT GGG TTT GAT CTT AAT      531
Thr Ile Ile Thr Arg Asn Leu Ile Tyr Lys Asp Gly Phe Asp Leu Asn
   80             85             90

AAA GGC ATT GAA GGA AAG ATA CGT ACG CAT TTG TCA GAG CAT TGT ACA      579
Lys Gly Ile Glu Gly Lys Ile Arg Thr His Leu Ser Glu His Cys Thr
   95             100            105

AAT GGA TCA GAA GTA CAA AGT CCA TGG ATA GAA GCT TCT TAT GGG ATA      627
Asn Gly Ser Glu Val Gln Ser Pro Trp Ile Glu Ala Ser Tyr Gly Ile
  110             115             120

TCA GAT GAA GGA AGT TTG GAA ACT AAA ATT CAG GAC ATG AAG TGT ATA      675
Ser Asp Glu Gly Ser Leu Glu Thr Lys Ile Gln Asp Met Lys Cys Ile
 125             130             135             140

TAT TAT AAC TGG CAG TAT TTG GTC TGC TCT TGG AAA CCT GGC AAG ACA      723
Tyr Tyr Asn Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Lys Thr
 145             150             155

GTA TAT TCT GAT ACC AAC TAT ACC ATG TTT TTC TGG TAT GAG GGC TTG      771
Val Tyr Ser Asp Thr Asn Tyr Thr Met Phe Phe Trp Tyr Glu Gly Leu
 160             165             170

GAT CAT GCC TTA CAG TGT GCT GAT TAC CTC CAG CAT GAT GAA AAA AAT      819
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Asp His Ala Leu Gln Cys Ala Asp Tyr Leu Gln His Asp Glu Lys Asn	
175 180 185	
GTT GGA TGC AAA CTG TCC AAC TTG GAC TCA TCA GAC TAT AAA GAT TTT	867
Val Gly Cys Lys Leu Ser Asn Leu Asp Ser Ser Asp Tyr Lys Asp Phe	
190 195 200	
TTT ATC TGT GTT AAT GGA TCT TCA AAG TTG GAA CCC ATC AGA TCC AGC	915
Phe Ile Cys Val Asn Gly Ser Ser Lys Leu Glu Pro Ile Arg Ser Ser	
205 210 215 220	
TAT ACA GTT TTT CAA CTT CAA AAT ATA GTT AAA CCA TTG CCA CCA GAA	963
Tyr Thr Val Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro Pro Glu	
225 230 235	
TTC CTT CAT ATT AGT GTG GAG AAT TCC ATT GAT ATT AGA ATG AAA TGG	1011
Phe Leu His Ile Ser Val Glu Asn Ser Ile Asp Ile Arg Met Lys Trp	
240 245 250	
AGC ACA CCT GGA GGA CCC ATT CCA CCA AGG TGT TAC ACT TAT GAA ATT	1059
Ser Thr Pro Gly Gly Pro Ile Pro Pro Arg Cys Tyr Thr Tyr Glu Ile	
255 260 265	
GTG ATC CGA GAA GAC GAT ATT TCC TGG GAG TCT GCC ACA GAC AAA AAC	1107
Val Ile Arg Glu Asp Asp Ile Ser Trp Glu Ser Ala Thr Asp Lys Asn	
270 275 280	
GAT ATG AAG TTG AAG AGG AGA GCA AAT GAA AGT GAA GAC CTA TGC TTT	1155
Asp Met Lys Leu Lys Arg Arg Ala Asn Glu Ser Glu Asp Leu Cys Phe	
285 290 295 300	
TTT GTA AGA TGT AAG GTC AAT ATA TAT TGT GCA GAT GAT GGA ATT TGG	1203
Phe Val Arg Cys Lys Val Asn Ile Tyr Cys Ala Asp Asp Gly Ile Trp	
305 310 315	
AGC GAA TGG AGT GAA GAG GAA TGT TGG GAA GGT TAC ACA GGG CCA GAC	1251
Ser Glu Trp Ser Glu Glu Glu Cys Trp Glu Gly Tyr Thr Gly Pro Asp	
320 325 330	
TCA AAG ATT ATT TTC ATA GTA CCA GTT TGT CTT TTC TTT ATA TTC CTT	1299
Ser Lys Ile Ile Phe Ile Val Pro Val Cys Leu Phe Phe Ile Phe Leu	
335 340 345	
TTG TTA CTT CTT TGC CTT ATT GTG GAG AAG GAA GAA CCT GAA CCC ACA	1347
Leu Leu Leu Leu Cys Leu Ile Val Glu Lys Glu Glu Pro Glu Pro Thr	
350 355 360	
TTG AGC CTC CAT GTG GAT CTG AAC AAA GAA GTG TGT GCT TAT GAA GAT	1395
Leu Ser Leu His Val Asp Leu Asn Lys Glu Val Cys Ala Tyr Glu Asp	
365 370 375 380	
ACC CTC TGT TAAACCACCA ATTTCTTGAC ATAGAGCCAG CCAGCAGGAG	1444
Thr Leu Cys	
TCATATTAAA CTCAATTTCT CTTAAATTT CGAATACATC TTCTTGAAAA TCCAAAAAAA	1504
AAAAAAAAAA AAAAACTCGA G	1525

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Ala Phe Val His Ile Arg Cys Leu Cys Phe Ile Leu Leu Cys Thr
 1             5             10             15
Ile Thr Gly Tyr Ser Leu Glu Ile Lys Val Asn Pro Pro Gln Asp Phe
 20             25             30
Glu Ile Leu Asp Pro Gly Leu Leu Gly Tyr Leu Tyr Leu Gln Trp Lys
 35             40             45
Pro Pro Val Val Ile Glu Lys Phe Lys Gly Cys Thr Leu Glu Tyr Glu
 50             55             60
Leu Lys Tyr Arg Asn Val Asp Ser Asp Ser Trp Lys Thr Ile Ile Thr
 65             70             75             80
Arg Asn Leu Ile Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile Glu
 85             90             95
Gly Lys Ile Arg Thr His Leu Ser Glu His Cys Thr Asn Gly Ser Glu
100            105            110
Val Gln Ser Pro Trp Ile Glu Ala Ser Tyr Gly Ile Ser Asp Glu Gly
115            120            125
Ser Leu Glu Thr Lys Ile Gln Asp Met Lys Cys Ile Tyr Tyr Asn Trp
130            135            140
Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Lys Thr Val Tyr Ser Asp
145            150            155            160
Thr Asn Tyr Thr Met Phe Phe Trp Tyr Glu Gly Leu Asp His Ala Leu
165            170            175
Gln Cys Ala Asp Tyr Leu Gln His Asp Glu Lys Asn Val Gly Cys Lys
180            185            190
Leu Ser Asn Leu Asp Ser Ser Asp Tyr Lys Asp Phe Phe Ile Cys Val
195            200            205
Asn Gly Ser Ser Lys Leu Glu Pro Ile Arg Ser Ser Tyr Thr Val Phe
210            215            220
Gln Leu Gln Asn Ile Val Lys Pro Leu Pro Pro Glu Phe Leu His Ile
225            230            235            240
Ser Val Glu Asn Ser Ile Asp Ile Arg Met Lys Trp Ser Thr Pro Gly
245            250            255
Gly Pro Ile Pro Pro Arg Cys Tyr Thr Tyr Glu Ile Val Ile Arg Glu
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260	265	270
Asp Asp Ile Ser Trp Glu Ser Ala Thr Asp Lys Asn Asp Met Lys Leu		
275	280	285
Lys Arg Arg Ala Asn Glu Ser Glu Asp Leu Cys Phe Phe Val Arg Cys		
290	295	300
Lys Val Asn Ile Tyr Cys Ala Asp Asp Gly Ile Trp Ser Glu Trp Ser		
305	310	315
Glu Glu Glu Cys Trp Glu Gly Tyr Thr Gly Pro Asp Ser Lys Ile Ile		
325	330	335
Phe Ile Val Pro Val Cys Leu Phe Phe Ile Phe Leu Leu Leu Leu Leu		
340	345	350
Cys Leu Ile Val Glu Lys Glu Glu Pro Glu Pro Thr Leu Ser Leu His		
355	360	365
Val Asp Leu Asn Lys Glu Val Cys Ala Tyr Glu Asp Thr Leu Cys		
370	375	380

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 103..1245

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGATCCGCGC GGATGAAGGC TATTTGAAGT CGCCATAACC TGGTCAGAAG TGTGCCTGTC	60
GGCGGGGAGA GAGGCAATAT CAAGGTTTTA AATCTCGGAG AA ATG GCT TTC GTT	114
Met Ala Phe Val	
1	
TGC TTG GCT ATC GGA TGC TTA TAT ACC TTT CTG ATA AGC ACA ACA TTT	162
Cys Leu Ala Ile Gly Cys Leu Tyr Thr Phe Leu Ile Ser Thr Thr Phe	
5 10 15 20	
GGC TGT ACT TCA TCT TCA GAC ACC GAG ATA AAA GTT AAC CCT CCT CAG	210
Gly Cys Thr Ser Ser Ser Asp Thr Glu Ile Lys Val Asn Pro Pro Gln	
25 30 35	
GAT TTT GAG ATA GTG GAT CCC GGA TAC TTA GGT TAT CTC TAT TTG CAA	258
Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Tyr Leu Gln	
40 45 50	

TGG CAA CCC CCA CTG TCT CTG GAT CAT TTT AAG GAA TGC ACA GTG GAA Trp Gln Pro Pro Leu Ser Leu Asp His Phe Lys Glu Cys Thr Val Glu 55 60 65	306
TAT GAA CTA AAA TAC CGA AAC ATT GGT AGT GAA ACA TGG AAG ACC ATC Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr Trp Lys Thr Ile 70 75 80	354
ATT ACT AAG AAT CTA CAT TAC AAA GAT GGG TTT GAT CTT AAC AAG GGC Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly 85 90 95 100	402
ATT GAA GCG AAG ATA CAC ACG CTT TTA CCA TGG CAA TGC ACA AAT GGA Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln Cys Thr Asn Gly 105 110 115	450
TCA GAA GTT CAA AGT TCC TGG GCA GAA ACT ACT TAT TGG ATA TCA CCA Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr Trp Ile Ser Pro 120 125 130	498
CAA GGA ATT CCA GAA ACT AAA GTT CAG GAT ATG GAT TGC GTA TAT TAC Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp Cys Val Tyr Tyr 135 140 145	546
AAT TGG CAA TAT TTA CTC TGT TCT TGG AAA CCT GGC ATA GGT GTA CTT Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly Ile Gly Val Leu 150 155 160	594
CTT GAT ACC AAT TAC AAC TTG TTT TAC TGG TAT GAG GGC TTG GAT CAT Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His 165 170 175 180	642
GCA TTA CAG TGT GTT GAT TAC ATC AAG GCT GAT GGA CAA AAT ATA GGA Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly Gln Asn Ile Gly 185 190 195	690
TGC AGA TTT CCC TAT TTG GAG GCA TCA GAC TAT AAA GAT TTC TAT ATT Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys Asp Phe Tyr Ile 200 205 210	738
TGT GTT AAT GGA TCA TCA GAG AAC AAG CCT ATC AGA TCC AGT TAT TTC Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg Ser Ser Tyr Phe 215 220 225	786
ACT TTT CAG CTT CAA AAT ATA GTT AAA CCT TTG CCG CCA GTC TAT CTT Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro Pro Val Tyr Leu 230 235 240	834
ACT TTT ACT CGG GAG AGT TCA TGT GAA ATT AAG CTG AAA TGG AGC ATA Thr Phe Thr Arg Glu Ser Ser Cys Glu Ile Lys Leu Lys Trp Ser Ile 245 250 255 260	882
CCT TTG GGA CCT ATT CCA GCA AGG TGT TTT GAT TAT GAA ATT GAG ATC Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Asp Tyr Glu Ile Glu Ile 265 270 275	930
AGA GAA GAT GAT ACT ACC TTG GTG ACT GCT ACA GTT GAA AAT GAA ACA Arg Glu Asp Asp Thr Thr Leu Val Thr Ala Thr Val Glu Asn Glu Thr 280 285 290	978

TAC ACC TTG AAA ACA ACA AAT GAA ACC CGA CAA TTA TGC TTT GTA GTA	1026
Tyr Thr Leu Lys Thr Thr Asn Glu Thr Arg Gln Leu Cys Phe Val Val	
295 300 305	
AGA AGC AAA GTG AAT ATT TAT TGC TCA GAT GAC GGA ATT TGG AGT GAG	1074
Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu	
310 315 320	
TGG AGT GAT AAA CAA TGC TGG GAA GGT GAA GAC CTA TCG AAG AAA ACT	1122
Trp Ser Asp Lys Gln Cys Trp Glu Gly Glu Asp Leu Ser Lys Lys Thr	
325 330 335 340	
TTG CTA CGT TTC TGG CTA CCA TTT GGT TTC ATC TTA ATA TTA GTT ATA	1170
Leu Leu Arg Phe Trp Leu Pro Phe Gly Phe Ile Leu Ile Leu Val Ile	
345 350 355	
TTT GTA ACC GGT CTG CTT TTG CGT AAG CCA AAC ACC TAC CCA AAA ATG	1218
Phe Val Thr Gly Leu Leu Leu Arg Lys Pro Asn Thr Tyr Pro Lys Met	
360 365 370	
ATT CCA GAA TTT TTC TGT GAT ACA TGA AGACTTTCCA TATCAAGAGA	1265
Ile Pro Glu Phe Phe Cys Asp Thr *	
375 380	
CATGGTATTG ACTCAACAGT TTCCAGTCAT GGCCAAATGT TCAATATGAG TCTCAATAAA	1325
CTGAATTTTT CTTGCGAAAA AAAAAAAAAA AAATCCGCGG ATCC	1369

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Phe Val Cys Leu Ala Ile Gly Cys Leu Tyr Thr Phe Leu Ile	
1 5 10 15	
Ser Thr Thr Phe Gly Cys Thr Ser Ser Ser Asp Thr Glu Ile Lys Val	
20 25 30	
Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr	
35 40 45	
Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser Leu Asp His Phe Lys Glu	
50 55 60	
Cys Thr Val Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr	
65 70 75 80	
Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp	
85 90 95	
Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln	
100 105 110	

Cys Thr Asn Gly Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr
 115 120 125
 Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp
 130 135 140
 Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly
 145 150 155 160
 Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu
 165 170 175
 Gly Leu Asp His Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly
 180 185 190
 Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys
 195 200 205
 Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg
 210 215 220
 Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro
 225 230 235 240
 Pro Val Tyr Leu Thr Phe Thr Arg Glu Ser Ser Cys Glu Ile Lys Leu
 245 250 255
 Lys Trp Ser Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Asp Tyr
 260 265 270
 Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr Leu Val Thr Ala Thr Val
 275 280 285
 Glu Asn Glu Thr Tyr Thr Leu Lys Thr Thr Asn Glu Thr Arg Gln Leu
 290 295 300
 Cys Phe Val Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly
 305 310 315 320
 Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys Trp Glu Gly Glu Asp Leu
 325 330 335
 Ser Lys Lys Thr Leu Leu Arg Phe Trp Leu Pro Phe Gly Phe Ile Leu
 340 345 350
 Ile Leu Val Ile Phe Val Thr Gly Leu Leu Leu Arg Lys Pro Asn Thr
 355 360 365
 Tyr Pro Lys Met Ile Pro Glu Phe Phe Cys Asp Thr *
 370 375 380

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

KSRTCCABK CRCTCCA

17

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATAGTTAAAC CATTGCCACC

20

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTCCATTTCG TCCTAAATTC

20

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AGTCTATCTT ACTTTTACTC G

21

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CATCTGAGCA ATAAATATTC AC

22